

In the specification:

Please amend the paragraph beginning at page 25, line 12 as follows:

-- To ensure that the cDNA fragments chosen will yield riboprobes specific only to the message of interest, a full homology search is performed for each potential message of interest. The names of the selected genes are searched in the NCBI database which is maintained by the National Institute of Health (NIH) (<http://www.ncbi.nlm.nih.gov/dbEST/index.html>). This database is a compilation of all known genes, their sequences, their discoverer, their sequencing orientation and other relevant information. Each entry is given a Genbank accession number which is used for identification purposes. This accession number is also used by various computer programs which link to the NCBI database for analysis of the DNA sequences, amino acid sequences, protein translations, and numerous other tasks. Versa Term PRO and Mac Vector, two programs which link to the NCBI database, were used to generate the information in Table 1. --